

# SEQUENCE LISTING

\*1100 Nicolaides, Nicholas C  
Grasso, Luigi  
Sass, Philip M

\*1200 METHODS FOR GENERATING GENETICALLY ALTERED  
ANTIBODY-PRODUCING CELL LINES WITH IMPROVED ANTIBODY  
CHARACTERISTICS

\*1300 MOR-0003

\*1400 00/000,000

\*1410 0000-11-07

\*1600 16

\*1700 PatentIn Ver. 2.1

\*2100 1

\*2110 14

\*2120 DNA

\*2130 Artificial Sequence

\*2200

\*2210 Description of Artificial Sequence:oligonucleotide  
primer

\*4000 1

ggaattttcag gtgcagattt tcag

24

\*2100 1

\*2110 11

\*2120 DNA

\*2130 Artificial Sequence

\*2200

\*2210 Description of Artificial Sequence:oligonucleotide  
primer

\*4000 2

actgcatagt gggaagatgg a

21

\*2100 1

\*2110 19

\*2120 DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
primer

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<211> 19

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 4

ttccatccc ccagtarwc

19

<210> 1

<211> 859

<212> FRT

<213> Mus musculus

<400> 1

Met Glu Gln Thr Glu Gly Val Ser Thr Glu Cys Ala Lys Ala Ile Lys  
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Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile  
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Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp  
35 40 45

Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp  
50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
65 70 75 80

Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser

100

105

110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser  
115 120 125

Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr  
130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln  
145 150 155 160

His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn  
165 170 175

Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys  
180 185 190

Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
195 200 205

Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys  
210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
225 230 235 240

Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly  
245 250 255

Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser  
260 265 270

Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser  
275 280 285

Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser  
290 295 300

Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
305 310 315 320

Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
340 345 350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn

355

360

365

Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
370 375 380

Val Lys Leu His Thr Ala Gln Leu Glu Lys Pro Val Pro Gly Lys Gln  
385 390 395 400

Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala  
405 410 415

Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu  
420 425 430

Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro  
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Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser  
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Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp  
465 470 475 480

Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly  
485 490 495

Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Glu Phe Ser Thr Pro Glu  
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Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp  
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Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro  
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Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys  
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565 570 575

Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro  
580 585 590

Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met  
595 600 605

Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys

610

615

620

Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu  
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Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala  
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Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu  
660 665 670

Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu  
675 680 685

Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr  
690 695 700

Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu  
705 710 715 720

Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu  
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Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile  
740 745 750

Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro  
755 760 765

Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile  
770 775 780

Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val  
785 790 795 800

Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly  
805 810 815

Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly  
820 825 830

Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg  
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His Val Ala Asn Leu Asp Val Ile Ser Gln Asn  
850 855

42100: 6  
42110: 3056  
42120: DNA  
42130: Mus musculus

44000: 6  
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 aqaactcaatt caaggacaaa aaaaaaaga tatttttgaa gccttttaaa aaaaaa 3056

4010: 7

4011: 862

4012: FRT

4013: Homo sapiens

4400: 7

Met Glu Arg Ala Glu Ser Ser Ser Thr Glu Pro Ala Lys Ala Ile Lys  
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Pro Ile Asp Arg Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Val  
 20 25 30

Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp  
 35 40 45

Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp  
 50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
 65 70 75 80

Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
 85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
 100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser  
 115 120 125

Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile  
 130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln  
 145 150 155 160

Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn

165

170

175

Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys  
180 185 190

Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
195 200 205

Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys  
210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
225 230 235 240

Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly  
245 250 255

Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe  
260 265 270

Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln  
275 280 285

Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg  
290 295 300

Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
305 310 315 320

Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
340 345 350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn  
355 360 365

Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
370 375 380

Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln  
385 390 395 400

Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser  
405 410 415

Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn



420

425

430

Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly  
 435 440 445

Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp  
 450 455 460

Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly  
 465 470 475 480

Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His  
 485 490 495

Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly  
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Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly  
 515 520 525

Ser Gln Glu His Val Asp Ser Gln Glu Lys Ala Pro Glu Thr Asp Asp  
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Ser Phe Ser Asp Val Asp Cys His Ser Asn Gln Glu Asp Thr Gly Cys  
 545 550 555 560

Lys Phe Arg Val Leu Pro Gln Pro Thr Asn Leu Ala Thr Pro Asn Thr  
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Lys Arg Phe Lys Lys Glu Glu Ile Leu Ser Ser Ser Asp Ile Cys Gln  
 580 585 590

Lys Leu Val Asn Thr Gln Asp Met Ser Ala Ser Gln Val Asp Val Ala  
 595 600 605

Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser  
 610 615 620

Leu Ala Lys Arg Ile Lys Gln Leu His His Glu Ala Gln Gln Ser Glu  
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Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu  
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Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met  
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Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile

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680

685

Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp  
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Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly  
705 710 715 720

Gln Arg Leu Ile Ala Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu  
725 730 735

Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp  
740 745 750

Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile  
755 760 765

Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp  
770 775 780

Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro  
785 790 795 800

Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val  
805 810 815

Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr  
820 825 830

His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro  
835 840 845

Thr Met Arg His Ile Ala Asn Leu Gly Val Ile Ser Gln Asn  
850 855 860

00100 -

00110 - 2771

00120 - DNA

00130 - Homo sapiens

0400 -

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(111) 932

(112) PFT

(113) Homo sapiens

<400> 9

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	210					215				220					
Phe	Gln	Tyr	His	Ser	Glu	Glu	Ser	Gln	Ile	Tyr	Leu	Ser	Gly	Phe	Leu
225				230						235				240	
Pro	Lys	Cys	Asp	Ala	Asp	His	Ser	Phe	Thr	Ser	Leu	Ser	Thr	Pro	Glu
			245						250					255	

Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile  
260 265 270

Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser  
275 280 285

Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala  
290 295 300

Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln  
305 310 315 320

Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys  
325 330 335

Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp  
340 345 350

Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val  
355 360 365

Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp  
370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly  
385 390 395 400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe  
405 410 415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr  
420 425 430

Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn  
435 440 445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His  
450 455 460

Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu  
465 470 475 480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp  
485 490 495

Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile  
500 505 510

Glu	Pro	Val	Lys	Ile	Leu	Val	Pro	Glu	Lys	Ser	Leu	Pro	Cys	Lys	Val	515	520	525
Ser	Asn	Asn	Asn	Tyr	Pro	Ile	Pro	Glu	Gln	Met	Asn	Leu	Asn	Glu	Asp	530	535	540
Ser	Cys	Asn	Lys	Lys	Ser	Asn	Val	Ile	Asp	Asn	Lys	Ser	Gly	Lys	Val	545	550	555
Thr	Ala	Tyr	Asp	Leu	Leu	Ser	Asn	Arg	Val	Ile	Lys	Lys	Pro	Met	Ser	565	570	575
Ala	Ser	Ala	Leu	Phe	Val	Gln	Asp	His	Arg	Pro	Gln	Phe	Leu	Ile	Glu	580	585	590
Asn	Pro	Lys	Thr	Ser	Leu	Glu	Asp	Ala	Thr	Leu	Gln	Ile	Glu	Glu	Leu	595	600	605
Trp	Lys	Thr	Leu	Ser	Glu	Glu	Glu	Lys	Leu	Lys	Tyr	Glu	Glu	Lys	Ala	610	615	620
Thr	Lys	Asp	Leu	Glu	Arg	Tyr	Asn	Ser	Gln	Met	Lys	Arg	Ala	Ile	Glu	625	630	635
Gln	Glu	Ser	Gln	Met	Ser	Leu	Lys	Asp	Gly	Arg	Lys	Lys	Ile	Lys	Pro	645	650	655
Thr	Ser	Ala	Trp	Asn	Leu	Ala	Gln	Lys	His	Lys	Leu	Lys	Thr	Ser	Leu	660	665	670
Ser	Asn	Gln	Pro	Lys	Leu	Asp	Glu	Leu	Leu	Gln	Ser	Gln	Ile	Glu	Lys	675	680	685
Arg	Arg	Ser	Gln	Asn	Ile	Lys	Met	Val	Gln	Ile	Pro	Phe	Ser	Met	Lys	690	695	700
Asn	Leu	Lys	Ile	Asn	Phe	Lys	Lys	Gln	Asn	Lys	Val	Asp	Leu	Glu	Glu	705	710	715
Lys	Asp	Glu	Pro	Cys	Leu	Ile	His	Asn	Leu	Arg	Phe	Pro	Asp	Ala	Trp	725	730	735
Leu	Met	Thr	Ser	Lys	Thr	Glu	Val	Met	Leu	Leu	Asn	Pro	Tyr	Arg	Val	740	745	750
Glu	Glu	Ala	Leu	Leu	Phe	Lys	Arg	Leu	Leu	Glu	Asn	His	Lys	Leu	Pro	755	760	765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn  
770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln  
785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn  
805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr  
820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala  
835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu  
850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu  
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp  
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile  
900 905 910

Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu  
915 920 925

Pro Glu Thr Thr  
930

4210 + 10

4211 + 3063

4212 + DNA

4213 + Homo sapiens

4400 + 10

ggcagcagtg gctgcttgog gctagtggat ggtaattgoc tgccctgcgcg tagcagcag 60  
ctgctctgtt aaaagcgaaa atgaaacaat tgcctgcgcg aacagttcga ctcttttcaa 120  
gttctcagat catcacttcg gtggtcagtg ttgtaaaaga gcttattgaa aactcttgg 180  
atgttggtgc cacaagcgtg gatgttaaac tggagaacta tggatttgat aaaattgagg 240  
tgcgagataa cggggagggt atcaaggctg ttgatgcacc tgtaattgca atgaagtaac 300  
aacctcaaaa aataaatagt catgaagatc ttgaaaattt gacaacttac ggttttcgtg 360  
gagaagcctt ggggtcaatt tgttgatatg ctgaggtttt aattacaaca agaaaggctg 420

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cttcacatct	tggtaaggt	acaaactgtaa	ctgctttaag	attatttaaa	aatctacotg	540
taagaaaagca	gttttaactca	actgcaaaaa	aatgttaaaga	tgaaataaaa	aagatccaaag	600
atctctctcat	gagctttggg	atccttaaaa	ctgaacttaag	gattgtcttt	gtacataaca	660
aggcagttat	ttggcagaaa	agcagagtat	cagatccaaa	gatggctctc	atctcagttc	720
tggggaactgc	tggttatgaac	aatatggaat	cttttcagta	ccactctgaa	gaktctcaga	780
tttatctcag	tggatttctt	ccaaagtgtg	atgcagacca	ctctttcaat	agctcttcaa	840
caccagaaaag	aagtttcctc	ttcataaaaa	gtgcacacag	acatcaaaaa	gattatctta	900
agttaatccg	acatcattac	aatctgaaat	gcttaaaagg	atctactctg	ttgtatctctg	960
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ccatgttcag	aagtgtctct	tttgttcaag	atcatctctc	tcagtctctc	atagaaaatc	1860
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aatgaagag	agccattgaa	caggagtcac	aaatgtcact	aaaagatggc	agaaaaaaga	2040
taaaaaccac	cagcgcattg	aatttcggcc	agaagcacaa	gttaaaaaac	tcattatcta	2100
atcaaccaaa	aattgatgaa	ctccttcagt	cccaaatgta	aaaaagaagg	agtcaaaaata	2160
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atgcctggct	aatgacatcc	aaaacagagg	taattgttatt	aaatccatat	agagtagaag	2340
aagccctgct	atttaaaaaga	cttcttgaga	atcataaaat	tcctgcagag	ccactggaaa	2400
agccaattat	gttaacagag	agtcttttta	atggacttca	ttatttagac	gttttatata	2460
aaatgacagc	agatgaccaa	agatacagtg	gatcaactta	ctgtctgat	ctccttotta	2520
cagcgaatgg	tttcaagata	aaattgatac	caggagtctc	aattactgaa	aattacttgg	2580
aatagaagg	aatggcta	tgtctcccat	tctatggagt	agcagattta	aaagaaattc	2640
ttaatgctat	attaaacaga	aatgcaagg	aagtttatga	atgtagacct	cgcgaagtga	2700
taagtatttt	agaggagaga	gcagtgcctc	tatccagaca	attacccatg	taattatcaa	2760
aagaggacat	ccaagacatt	atctacagaa	tgaagcacca	gtttggaaat	gaaattaaag	2820
agtgtgttca	tggctgcaca	ttttttcact	atttaacctc	tcttcagaa	actacatgat	2880
taaaatgtt	taagaagatt	agttaccatt	gaaattgggt	ctgtcataaa	acagcatgag	2940
tctgttttta	aattatcttt	gtattatgtg	tcacatgggt	attttttaaa	tgaggattca	3000
ctgacttggt	tttatattga	aaaaagttcc	acgtattgta	gaaaacgtaa	ataaactaat	3060
aac						3120



02110 934

02120 PRT

02130 Homo sapiens

04000 11

Met Ala Val Gln Pro Lys Glu Thr Leu Gln Leu Glu Ser Ala Ala Glu  
1 5 10 15

Val Gly Phe Val Arg Phe Phe Gln Gly Met Pro Glu Lys Pro Thr Thr  
20 25 30

Thr Val Arg Leu Phe Asp Arg Gly Asp Phe Tyr Thr Ala His Gly Glu  
35 40 45

Asp Ala Leu Leu Ala Ala Arg Glu Val Phe Lys Thr Gln Gly Val Ile  
50 55 60

Lys Tyr Met Gly Pro Ala Gly Ala Lys Asn Leu Gln Ser Val Val Leu  
65 70 75 80

Ser Lys Met Asn Phe Glu Ser Phe Val Lys Asp Leu Leu Leu Val Arg  
85 90 95

Gln Tyr Arg Val Glu Val Tyr Lys Asn Arg Ala Gly Asn Lys Ala Ser  
100 105 110

Lys Glu Asn Asp Trp Tyr Leu Ala Tyr Lys Ala Ser Pro Gly Asn Leu  
115 120 125

Ser Gln Phe Glu Asp Ile Leu Phe Gly Asn Asn Asp Met Ser Ala Ser  
130 135 140

Ile Gly Val Val Gly Val Lys Met Ser Ala Val Asp Gly Gln Arg Gln  
145 150 155 160

Val Gly Val Gly Tyr Val Asp Ser Ile Gln Arg Lys Leu Gly Leu Cys  
165 170 175

Glu Phe Pro Asp Asn Asp Gln Phe Ser Asn Leu Glu Ala Leu Leu Ile  
180 185 190

Gln Ile Gly Pro Lys Glu Cys Val Leu Pro Gly Gly Glu Thr Ala Gly  
195 200 205

Asp Met Gly Lys Leu Arg Gln Ile Ile Gln Arg Gly Gly Ile Leu Ile  
210 215 220

Thr Glu Arg Lys Lys Ala Asp Phe Ser Thr Lys Asp Ile Tyr Gln Asp

225

230

235

240

Leu Asn Arg Leu Leu Lys Gly Lys Lys Gly Glu Gln Met Asn Ser Ala  
 245 250 255

Val Leu Pro Glu Met Glu Asn Gln Val Ala Val Ser Ser Leu Ser Ala  
 260 265 270

Val Ile Lys Phe Leu Glu Leu Leu Ser Asp Asp Ser Asn Phe Gly Gln  
 275 280 285

Phe Glu Leu Thr Thr Phe Asp Phe Ser Gln Tyr Met Lys Leu Asp Ile  
 290 295 300

Ala Ala Val Arg Ala Leu Asn Leu Phe Gln Gly Ser Val Glu Asp Thr  
 305 310 315 320

Thr Gly Ser Gln Ser Leu Ala Ala Leu Leu Asn Lys Cys Lys Thr Pro  
 325 330 335

Gln Gly Gln Arg Leu Val Asn Gln Trp Ile Lys Gln Pro Leu Met Asp  
 340 345 350

Lys Asn Arg Ile Glu Glu Arg Leu Asn Leu Val Glu Ala Phe Val Glu  
 355 360 365

Asp Ala Glu Leu Arg Gln Thr Leu Gln Glu Asp Leu Leu Arg Arg Phe  
 370 375 380

Pro Asp Leu Asn Arg Leu Ala Lys Lys Phe Gln Arg Gln Ala Ala Asn  
 385 390 395 400

Leu Gln Asp Cys Tyr Arg Leu Tyr Gln Gly Ile Asn Gln Leu Pro Asn  
 405 410 415

Val Ile Gln Ala Leu Glu Lys His Glu Gly Lys His Gln Lys Leu Leu  
 420 425 430

Leu Ala Val Phe Val Thr Pro Leu Thr Asp Leu Arg Ser Asp Phe Ser  
 435 440 445

Lys Phe Gln Glu Met Ile Glu Thr Thr Leu Asp Met Asp Gln Val Glu  
 450 455 460

Asn His Glu Phe Leu Val Lys Pro Ser Phe Asp Pro Asn Leu Ser Glu  
 465 470 475 480

Leu Arg Glu Ile Met Asn Asp Leu Glu Lys Lys Met Gln Ser Thr Leu

Ile Ser Ala Ala Arg Asp Leu Gly Leu Asp Pro Gly Lys Gln Ile Lys  
500 505 510

Leu Asp Ser Ser Ala Gln Phe Gly Tyr Tyr Phe Arg Val Thr Cys Lys  
515 520 525

Glu Glu Lys Val Leu Arg Asn Asn Lys Asn Phe Ser Thr Val Asp Ile  
530 535 540

Gln Lys Asn Gly Val Lys Phe Thr Asn Ser Lys Leu Thr Ser Leu Asn  
545 550 555 560

Glu Glu Tyr Thr Lys Asn Lys Thr Glu Tyr Glu Glu Ala Gln Asp Ala  
565 570 575

Ile Val Lys Glu Ile Val Asn Ile Ser Ser Gly Tyr Val Glu Pro Met  
580 585 590

Gln Thr Leu Asn Asp Val Leu Ala Gln Leu Asp Ala Val Val Ser Phe  
595 600 605

Ala His Val Ser Asn Gly Ala Pro Val Pro Tyr Val Arg Pro Ala Ile  
610 615 620

Leu Glu Lys Gly Gln Gly Arg Ile Ile Leu Lys Ala Ser Arg His Ala  
625 630 635 640

Cys Val Glu Val Gln Asp Glu Ile Ala Phe Ile Pro Asn Asp Val Tyr  
645 650 655

Phe Glu Lys Asp Lys Gln Met Phe His Ile Ile Thr Gly Pro Asn Met  
660 665 670

Gly Gly Lys Ser Thr Tyr Ile Arg Gln Thr Gly Val Ile Val Leu Met  
675 680 685

Ala Gln Ile Gly Cys Phe Val Pro Cys Glu Ser Ala Glu Val Ser Ile  
690 695 700

Val Asp Cys Ile Leu Ala Arg Val Gly Ala Gly Asp Ser Gln Leu Lys  
705 710 715 720

Gly Val Ser Thr Phe Met Ala Glu Met Leu Gln Thr Ala Ser Ile Leu  
725 730 735

Arg Ser Ala Thr Lys Asp Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg

740

745

750

Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Ser Glu  
755 760 765

Tyr Ile Ala Thr Lys Ile Gly Ala Phe Cys Met Phe Ala Thr His Phe  
770 775 780

His Glu Leu Thr Ala Leu Ala Asn Gln Ile Pro Thr Val Asn Asn Leu  
785 790 795 800

His Val Thr Ala Leu Thr Thr Glu Glu Thr Leu Thr Met Leu Tyr Gln  
805 810 815

Val Lys Lys Gly Val Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu  
820 825 830

Leu Ala Asn Phe Pro Lys His Val Ile Glu Cys Ala Lys Gln Lys Ala  
835 840 845

Leu Glu Leu Glu Glu Phe Gln Tyr Ile Gly Glu Ser Gln Gly Tyr Asp  
850 855 860

Ile Met Glu Pro Ala Ala Lys Lys Cys Tyr Leu Glu Arg Glu Gln Gly  
865 870 875 880

Glu Lys Ile Ile Gln Glu Phe Leu Ser Lys Val Lys Gln Met Pro Phe  
885 890 895

Thr Glu Met Ser Glu Glu Asn Ile Thr Ile Lys Leu Lys Gln Leu Lys  
900 905 910

Ala Glu Val Ile Ala Lys Asn Asn Ser Phe Val Asn Glu Ile Ile Ser  
915 920 925

Arg Ile Lys Val Thr Thr  
930

0010 12

0011 3145

0012 DNA

0013 Homo sapiens

0400 12

ggcgggaaac agcttagtgg gtgtgggggtc ggcgattttc ttcaaccagg aggtgaggag 60  
gtttcgacat ggcgggtgcag ccgaaggaga cgtgcagtt ggagagcgcg gcgaggtcg 120  
gtttgtgog cttcttttcag ggcattgcgg agaagccgac caccacagtg cgccttttcg 180

acggggggga	ttttatatac	gggcaaggog	aggacggogt	gotgggogoo	ggggagggtg	213
tcaagaccca	gggggtgato	aagtaacatg	ggcgggcagg	agcaaaagaat	ctgcagagtg	311
ttgtgottag	taaaatgaat	tttgaatott	ttgtaaaaga	tottottotg	gttcgtcagt	370
atagagttga	agtttataag	aatagagotg	gaaataaggo	atccaaggag	aatgattggt	413
atttggcata	taaggottot	cctggcaatc	tctctcagtt	tgaagacatt	ctcttttgta	417
acaatgatat	gtcagottoc	attgggtgtg	tgggtgttaa	aatgtccgca	gttgatggoo	543
agagacaggt	tggagttggg	tatgtggatt	ccatacagag	gaaaactagga	ctgtgtgaat	611
tccttgataa	tgatcagttc	tccaattttg	aggetctctc	cattccagatt	ggaccaagg	663
aatgtgtttt	acccggagga	gagactgtct	gagacatggg	gaaaactgaga	cagataattt	713
aaagaggagg	aattctgato	acagaaagaa	aaaaagctga	cttttccaca	aaagacattt	741
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tgcacagaaat	gcagaatcag	gttgcagttt	catactgttc	tgcggttaac	aagtttttag	911
aactcttata	agatgattoc	aacttttgac	agtttgaact	gactactctt	gaatttcagc	970
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cagtaatgga	atgaaggtaa	tattgataag	ctattgtctg	taatagtttt	atattgtttt	2940
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. gctgttaactg aggaactgttt gcaattgaca taggcaataa taagtgatgt gotgaatttt 3120  
 ataaataaaa tcatgtagtt tgtgg 3145

02100 13  
 02110 756  
 02120 PRT  
 02130 Homo sapiens

04000 13  
 Met Ser Phe Val Ala Gly Val Ile Arg Arg Leu Asp Glu Thr Val Val  
 1 5 10 15  
 Asn Arg Ile Ala Ala Gly Glu Val Ile Gln Arg Pro Ala Asn Ala Ile  
 20 25 30  
 Lys Glu Met Ile Glu Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Gln  
 35 40 45  
 Val Ile Val Lys Glu Gly Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn  
 50 55 60  
 Gly Thr Gly Ile Arg Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe  
 65 70 75 80  
 Thr Thr Ser Lys Leu Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr  
 85 90 95  
 Tyr Gly Phe Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala His  
 100 105 110  
 Val Thr Ile Thr Thr Lys Thr Ala Asp Gly Lys Cys Ala Tyr Arg Ala  
 115 120 125  
 Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly  
 130 135 140  
 Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala  
 145 150 155 160  
 Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile  
 165 170 175  
 Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe  
 180 185 190  
 Ser Val Lys Lys Gln Gly Glu Thr Val Ala Asp Val Arg Thr Leu Pro  
 195 200 205

Asn Ala Ser Thr Val Asp Asn Ile Arg Ser Ile Phe Gly Asn Ala Val  
210 215 220

Ser Arg Glu Leu Ile Glu Ile Gly Cys Glu Asp Lys Thr Leu Ala Phe  
225 230 235 240

Lys Met Asn Gly Tyr Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys  
245 250 255

Ile Phe Leu Leu Phe Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu  
260 265 270

Arg Lys Ala Ile Glu Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr  
275 280 285

His Pro Phe Leu Tyr Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp  
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Val Asn Val His Pro Thr Lys His Glu Val His Phe Leu His Glu Glu  
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Ser Ile Leu Glu Arg Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly  
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Ala Gly Pro Ser Gly Glu Met Val Lys Ser Thr Thr Ser Leu Thr Ser  
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Arg Thr Asp Ser Arg Glu Gln Lys Leu Asp Ala Phe Leu Gln Pro Leu  
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Glu Leu Pro Ala Pro Ala Glu Val Ala Ala Lys Asn Gln Ser Leu Glu  
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Ile Asn Glu Gln Gly His Glu Val Leu Arg Glu Met Leu His Asn His  
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Thr Lys Leu Tyr Leu Leu Asn Thr Thr Lys Leu Ser Glu Glu Leu Phe  
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Tyr Gln Ile Leu Ile Tyr Asp Phe Ala Asn Phe Gly Val Leu Arg Leu  
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Tyr Phe Ser Leu Glu Ile Asp Glu Glu Gly Asn Leu Ile Gly Leu Pro  
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Leu Leu Ile Asp Asn Tyr Val Pro Pro Leu Glu Gly Leu Pro Ile Phe  
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Phe Glu Ser Leu Ser Lys Glu Cys Ala Met Phe Tyr Ser Ile Arg Lys  
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Gln Tyr Ile Ser Glu Glu Ser Thr Leu Ser Gly Gln Gln Ser Glu Val  
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Pro Gly Ser Ile Pro Asn Ser Trp Lys Trp Thr Val Glu His Ile Val  
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Tyr Lys Ala Leu Arg Ser His Ile Leu Pro Pro Lys His Phe Thr Glu  
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Asp Gly Asn Ile Leu Gln Leu Ala Asn Leu Pro Asp Leu Tyr Lys Val  
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Phe Glu Arg Cys  
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02120: DNA  
02130: Homo sapiens

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<213> Homo sapiens

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Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp

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Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe

65 70 75 80

Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala

85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser

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Ala Lys Val Gly Thr

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